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OM protein - protein search, using sw model

Run on: October 3, 2005, 11:44:09 ; Search time 164 Seconds  
(without alignments)  
551.801 Million cell updates/sec

Title: US-10-694-978-2  
Perfect score: 218  
Sequence: 1 MSFVGENSGVMGSEDMEND.....IEFSFQVCKRAEMSPSEVSD 218

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1846076 seqs, 415116000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :

- Published Applications AA:\*
- 1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*
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  - 3: /cgn2\_6/prodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/prodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
  - 5: /cgn2\_6/prodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
  - 6: /cgn2\_6/prodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
  - 7: /cgn2\_6/prodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
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  - 10: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*
  - 11: /cgn2\_6/prodata/1/pubppaa/US09C\_PUBCOMB.pep:\*
  - 12: /cgn2\_6/prodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
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  - 16: /cgn2\_6/prodata/1/pubppaa/US10D\_PUBCOMB.pep:\*
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  - 19: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep:\*
  - 20: /cgn2\_6/prodata/1/pubppaa/US11\_NEW\_PUB.pep:\*
  - 21: /cgn2\_6/prodata/1/pubppaa/US60\_NEW\_PUB.pep:\*
  - 22: /cgn2\_6/prodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	218	100.0	218	US-10-695-195-2
2	218	100.0	218	US-10-694-978-2
3	65	29.8	176	US-09-965-528-25
4	65	29.8	176	US-09-969-984-25
5	55	25.2	115	US-10-095-407-5
6	55	25.2	115	US-10-095-407-9
7	55	25.2	115	US-10-095-407-13
8	55	25.2	136	US-10-095-407-11
9	55	25.2	157	US-09-876-790-10
10	55	25.2	157	US-10-302-554-9
11	55	25.2	157	US-10-302-554-15

12	55	25.2	157	US-10-888-918-10	Sequence 10, Appl
13	55	25.2	157	US-10-888-867-10	Sequence 10, Appl
14	55	25.2	157	US-10-888-779-10	Sequence 10, Appl
15	55	25.2	157	US-10-888-780-10	Sequence 10, Appl
16	55	25.2	157	US-10-888-931-10	Sequence 10, Appl
17	55	25.2	167	US-10-095-407-7	Sequence 7, Appl1
18	55	25.2	178	US-10-095-407-2	Sequence 11, Appl1
19	55	25.2	178	US-10-139-833-11	Sequence 3, Appl1
20	55	25.2	192	US-09-876-790-3	Sequence 13, Appl1
21	55	25.2	192	US-10-139-833-13	Sequence 3, Appl1
22	55	25.2	192	US-10-888-918-3	Sequence 3, Appl1
23	55	25.2	192	US-10-888-867-3	Sequence 3, Appl1
24	55	25.2	192	US-10-888-779-3	Sequence 3, Appl1
25	55	25.2	192	US-10-888-780-3	Sequence 3, Appl1
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27	55	25.2	193	US-10-063-512-142	Sequence 142, App
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54	55	25.2	193	US-10-063-526-142	Sequence 142, App
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56	55	25.2	193	US-10-063-546-142	Sequence 142, App
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64	55	25.2	193	US-10-063-674-142	Sequence 142, App
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126	55	25.2	193	14	US-10-063-528-142	Sequence 142, App
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147	55	25.2	193	14	US-10-063-536-142	Sequence 142, App
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149	55	25.2	193	14	US-10-063-638-142	Sequence 142, App
150	55	25.2	193	14	US-10-063-666-142	Sequence 142, App

## ALIGNMENTS

Sequence 2, Application US/10695195  
Publication No. US20040068099A1  
GENERAL INFORMATION:  
APPLICANT: Timans, Jacqueline C.  
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/695,195  
FILING DATE: 27-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,412  
FILING DATE: 17-Sep-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0904K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-9196  
TELEFAX: (650) 496-1200  
INFORMATION FOR SEQ ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-695-195-2

Query Match 100.0%; Score 218; DB 15; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1.2e-199;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSFVGENSGVKGWSEMEKDEPOCCLEDPAGSPLEPGSPLEPTMNFVHTRKYSLNPKKF	60
DB	1	MSFVGENSGVKGWSEMEKDEPOCCLEDPAGSPLEPGSPLEPTMNFVHTRKYSLNPKKF	60
QY	61	SHHDQHKVLDVDSGNLIVAPDKNYIRPEIFPALASLSSASAEKSGSLILGVSKGEFCL	120
DB	61	SHHDQHKVLDVDSGNLIVAPDKNYIRPEIFPALASLSSASAEKSGSLILGVSKGEFCL	120
QY	121	YCKKDGQGHSPISQLEKKEIKMLAOKESARRPIFYRAOVGSRRNMLEAHPGWFICTS	180
DB	121	YCKKDGQGHSPISQLEKKEIKMLAOKESARRPIFYRAOVGSRRNMLEAHPGWFICTS	180
QY	181	CNCEPVGVTDKPENRKHIEFSFOPVCKAEMSPSEVSD	218
DB	181	CNCEPVGVTDKPENRKHIEFSFOPVCKAEMSPSEVSD	218

RESULT 2  
US-10-694-978-2  
Sequence 2, Application US/10694978  
Publication No. US2004008776A1  
GENERAL INFORMATION:  
APPLICANT: Timans, Jacqueline C.  
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue

CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/694,978  
FILING DATE: 27-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,412  
FILING DATE: 17-Sep-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0904K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-694-978-2

Query Match 100.0%; Score 218; DB 15; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1.2e-199; Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MSFVGENSGVGMGSEDEKDEPOCCLEDPAGSPLEPPSPLEPTMNFVTSRKVSLNPKKF 60  
QY 61 SHDQHKVLDGSLIAVPDKNYIRPEIFPALASSLSASAKGSLILLGVSKGEFCL 120  
DB 61 SHDQHKVLDGSLIAVPDKNYIRPEIFPALASSLSASAKGSLILLGVSKGEFCL 120  
QY 121 YCDKDKQSHPSIOLKKEKMKLAQKESARPRITFRAOVGSNNMESAAHPWFICTS 180  
DB 121 YCDKDKQSHPSIOLKKEKMKLAQKESARPRITFRAOVGSNNMESAAHPWFICTS 180  
QY 181 CNCNEPVGVTDKFENRKHIEFSFOVCKAEMSPSEVSD 218  
DB 181 CNCNEPVGVTDKFENRKHIEFSFOVCKAEMSPSEVSD 218

RESULT 3  
US-09-965-528-25  
Sequence 25, Application US/09965528  
Publication No. US20020187523A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.  
APPLICANT: TANG, Y. Tom  
APPLICANT: YUE, Henry  
APPLICANT: LAL, Preeti  
APPLICANT: BURFORD, Neil  
APPLICANT: BANDMAN, Olga  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: LU, Dzung Aina M.  
APPLICANT: PATTERSON, Chandra  
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES  
FILE REFERENCE: PF-0701 USA  
CURRENT APPLICATION NUMBER: US/09/965,528  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/134,949

PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 60/144,270  
PRIOR FILING DATE: 1999-07-15  
PRIOR APPLICATION NUMBER: 60/146,700  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 60/157,508  
PRIOR FILING DATE: 1999-10-04  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PERL Program  
SEQ ID NO 25  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20020187523A1 4365383CD1  
US-09-965-528-25

Query Match 29.8%; Score 65; DB 9; Length 176;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53; Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MNFVTSRKVKSINPKKFSIHDDHKVLDGSLIAVPDKNYIRPEIFPALASSLSAS 102  
DB 1 MNFVTSRKVKSINPKKFSIHDDHKVLDGSLIAVPDKNYIRPEIFPALASSLSAS 60  
QY 103 AEKGS 107  
DB 61 AEKGS 65

RESULT 4  
US-09-969-984-25  
Sequence 25, Application US/09969984  
Publication No. US20040048244A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.  
APPLICANT: TANG, Y. Tom  
APPLICANT: YUE, Henry  
APPLICANT: LAL, Preeti  
APPLICANT: BURFORD, Neil  
APPLICANT: BANDMAN, Olga  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: LU, Dzung Aina M.  
APPLICANT: PATTERSON, Chandra  
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES  
FILE REFERENCE: PF-0701-1 USA  
CURRENT APPLICATION NUMBER: US/09/969,984  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508  
PRIOR FILING DATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PERL Program  
SEQ ID NO 25  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040048244A1 4365383CD1  
US-09-969-984-25

Query Match 29.8%; Score 65; DB 11; Length 176;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53; Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MNFVTSRKVKSINPKKFSIHDDHKVLDGSLIAVPDKNYIRPEIFPALASSLSAS 102  
DB 1 MNFVTSRKVKSINPKKFSIHDDHKVLDGSLIAVPDKNYIRPEIFPALASSLSAS 60  
QY 103 AEKGS 107  
DB 61 AEKGS 65

Db 61 AEXGS 65

RESULT 5

US-10-095-407-5

Sequence 5, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-10-095-407-5

Query Match 25.2%; Score 55; DB 13; Length 115;

Best Local Similarity 100.0%; Pred. No. 3.2e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163

6 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 60

RESULT 6

US-10-095-407-9

Sequence 9, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 9

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-10-095-407-9

Query Match 25.2%; Score 55; DB 13; Length 115;

Best Local Similarity 100.0%; Pred. No. 3.2e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163

6 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 60

RESULT 7

US-10-095-407-13

Sequence 13, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-10-095-407-13

Query Match 25.2%; Score 55; DB 13; Length 115;

Best Local Similarity 100.0%; Pred. No. 3.2e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163

6 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 60

RESULT 8

US-10-095-407-11

Sequence 11, Application US/10095407

Publication No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: US 60/054,646

PRIOR FILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 11

LENGTH: 136

TYPE: PRT

ORGANISM: Homo sapiens

US-10-095-407-11

Query Match 25.2%; Score 55; DB 13; Length 136;

Best Local Similarity 100.0%; Pred. No. 3.7e-44;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163

27 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 81

RESULT 9

US-09-876-790-10

Sequence 10, Application US/09876790

Publication No. US20030091532A1

GENERAL INFORMATION:

APPLICANT: SIMS, John E.

APPLICANT: SMITH, Dirk E.

APPLICANT: BORN, Teresa L.

TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTID

FILE REFERENCE: 2008-US

CURRENT APPLICATION NUMBER: US/09/876,790

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 60/112,163

PRIOR FILING DATE: 1998-12-14

PRIOR APPLICATION NUMBER: 60/146,675

;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/29549  
;; PRIOR FILING DATE: 1999-12-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 10  
;; LENGTH: 157  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-876-790-10

Query Match 25.2%; Score 55; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 102

RESULT 10  
US-10-302-554-9  
; Sequence 9, Application US/10302554  
; Publication No. US20030148467A1  
; GENERAL INFORMATION:  
; APPLICANT: West, Robert R.  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4  
; FILE REFERENCE: 98-59  
; CURRENT APPLICATION NUMBER: US/10/302,554  
; PRIOR FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US/09/428,118  
; PRIOR FILING DATE: 1999-10-27  
; PRIOR APPLICATION NUMBER: US 60/105,824  
; PRIOR FILING DATE: 1998-10-27  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-302-554-9

Query Match 25.2%; Score 55; DB 14; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 102

RESULT 11  
US-10-302-554-15  
; Sequence 15, Application US/10302554  
; Publication No. US20030148467A1  
; GENERAL INFORMATION:  
; APPLICANT: West, Robert R.  
; APPLICANT: Shepard, Paul O.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4  
; FILE REFERENCE: 98-59  
; CURRENT APPLICATION NUMBER: US/10/302,554  
; PRIOR FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: US/09/428,118  
; PRIOR FILING DATE: 1999-10-27  
; PRIOR APPLICATION NUMBER: US 60/105,824  
; PRIOR FILING DATE: 1998-10-27  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 157

;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: variant protein  
US-10-302-554-15

Query Match 25.2%; Score 55; DB 14; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 102

RESULT 12  
US-10-888-918-10  
; Sequence 10, Application US/10888918  
; Publication No. US20040248187A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,918  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-888-918-10

Query Match 25.2%; Score 55; DB 16; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 102

RESULT 13  
US-10-888-867-10  
; Sequence 10, Application US/10888867  
; Publication No. US2005009075A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMS, John E.  
; APPLICANT: SMITH, Dirk E.  
; APPLICANT: BORN, Teresa L.  
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI  
; FILE REFERENCE: 2008-US  
; CURRENT APPLICATION NUMBER: US/10/888,867  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/09/876,790  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/112,163  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: 60/146,675  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/29549  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 15

/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 10  
/ LENGTH: 157  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-888-867-10

Query Match 25.2%; Score 55; DB 17; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 14  
US-10-888-779-10  
/ Sequence 10, Application US/10888779  
/ Publication No. US2005009138A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMS, John E.  
/ APPLICANT: SMITH, Dirk E.  
/ APPLICANT: BORN, Teresa L.  
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAs AND POLYPEPTI  
/ FILE REFERENCE: 2008-US  
/ CURRENT APPLICATION NUMBER: US/10/888, 779  
/ CURRENT FILING DATE: 2004-07-09  
/ PRIOR APPLICATION NUMBER: US/09/876, 790  
/ PRIOR FILING DATE: 2001-06-06  
/ PRIOR APPLICATION NUMBER: 60/112,163  
/ PRIOR FILING DATE: 1998-12-14  
/ PRIOR APPLICATION NUMBER: 60/146,675  
/ PRIOR FILING DATE: 1999-11-10  
/ PRIOR APPLICATION NUMBER: PCT/US99/29549  
/ PRIOR FILING DATE: 1999-12-14  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 10  
/ LENGTH: 157  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-888-779-10

Query Match 25.2%; Score 55; DB 17; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 15  
US-10-888-780-10  
/ Sequence 10, Application US/10888780  
/ Publication No. US20050013797A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMS, John E.  
/ APPLICANT: SMITH, Dirk E.  
/ APPLICANT: BORN, Teresa L.  
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAs AND POLYPEPTI  
/ FILE REFERENCE: 2008-US  
/ CURRENT APPLICATION NUMBER: US/10/888, 780  
/ CURRENT FILING DATE: 2004-07-09  
/ PRIOR APPLICATION NUMBER: US/09/876, 790  
/ PRIOR FILING DATE: 2001-06-06  
/ PRIOR APPLICATION NUMBER: 60/112,163  
/ PRIOR FILING DATE: 1998-12-14  
/ PRIOR APPLICATION NUMBER: 60/146,675  
/ PRIOR FILING DATE: 1999-11-10  
/ PRIOR APPLICATION NUMBER: PCT/US99/29549  
/ PRIOR FILING DATE: 1999-12-14

/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 10  
/ LENGTH: 157  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-888-780-10

Query Match 25.2%; Score 55; DB 17; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 16  
US-10-888-931-10  
/ Sequence 10, Application US/10888931  
/ Publication No. US20050013798A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMS, John E.  
/ APPLICANT: SMITH, Dirk E.  
/ APPLICANT: BORN, Teresa L.  
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XREC2 DNAs AND POLYPEPTI  
/ FILE REFERENCE: 2008-US  
/ CURRENT APPLICATION NUMBER: US/10/888, 931  
/ CURRENT FILING DATE: 2004-07-09  
/ PRIOR APPLICATION NUMBER: US/09/876, 790  
/ PRIOR FILING DATE: 2001-06-06  
/ PRIOR APPLICATION NUMBER: 60/112,163  
/ PRIOR FILING DATE: 1998-12-14  
/ PRIOR APPLICATION NUMBER: 60/146,675  
/ PRIOR FILING DATE: 1999-11-10  
/ PRIOR APPLICATION NUMBER: PCT/US99/29549  
/ PRIOR FILING DATE: 1999-12-14  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 10  
/ LENGTH: 157  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-888-931-10

Query Match 25.2%; Score 55; DB 17; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.1e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
Db 48 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 102

RESULT 17  
US-10-095-407-7  
/ Sequence 7, Application US/10095407  
/ Publication No. US20020164330A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Pan, Yang  
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
/ TITLE OF INVENTION: AND USES THEREOF  
/ FILE REFERENCE: 09404/052001  
/ CURRENT APPLICATION NUMBER: US/10/095,407  
/ CURRENT FILING DATE: 2002-03-11  
/ PRIOR APPLICATION NUMBER: US 60/091,650  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: US 60/054,646  
/ PRIOR FILING DATE: 1997-08-04  
/ NUMBER OF SEQ ID NOS: 18  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 7  
/ LENGTH: 167

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-095-407-7

Query Match 25.2%; Score 55; DB 13; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.4e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163  
DB 58 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 112

## RESULT 18

US-10-095-407-2  
Sequence 2, Application US/10095407  
Publication No. US20020164330A1  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/10/095,407  
CURRENT FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/091,650  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: US 60/054,646  
PRIOR FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 178  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-095-407-2

Query Match 25.2%; Score 55; DB 13; Length 178;  
Best Local Similarity 100.0%; Pred. No. 4.6e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163  
DB 69 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 123

RESULT 19  
US-10-139-833-11  
Sequence 11, Application US/10139833  
Publication No. US20030004106A1  
GENERAL INFORMATION:  
APPLICANT: Sarris, Christiaan M.  
APPLICANT: Giles, Jennifer  
APPLICANT: Mu, Sharon X.  
APPLICANT: Xia, Min  
APPLICANT: Baes, Michael B.  
APPLICANT: Craveiro, Roger  
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and  
TITLE OF INVENTION: Uses Thereof  
FILE REFERENCE: 00-1213-E  
CURRENT APPLICATION NUMBER: US/10/139,833  
CURRENT FILING DATE: 2002-05-06  
PRIOR APPLICATION NUMBER: 60/170,191  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: 60/188,053  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: 60/194,521  
PRIOR FILING DATE: 2000-04-04  
PRIOR APPLICATION NUMBER: 60/195,910  
PRIOR FILING DATE: 2000-04-10  
PRIOR APPLICATION NUMBER: 09/724,583  
PRIOR FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11  
LENGTH: 178  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-139-833-11

Query Match 25.2%; Score 55; DB 14; Length 178;  
Best Local Similarity 100.0%; Pred. No. 4.6e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163  
DB 69 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 123

## RESULT 20

US-09-876-790-3  
Sequence 3, Application US/09876790  
Publication No. US20030091532A1  
GENERAL INFORMATION:  
APPLICANT: SIMS, John E.  
APPLICANT: SMITH, Dirk E.  
APPLICANT: BORN, Teresa L.  
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XREC2 DNAS AND POLYPEPTI  
FILE REFERENCE: 2008-US  
CURRENT APPLICATION NUMBER: US/09/876,790  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: 60/112,163  
PRIOR FILING DATE: 1998-12-14  
PRIOR APPLICATION NUMBER: 60/146,675  
PRIOR FILING DATE: 1999-11-10  
PRIOR APPLICATION NUMBER: PCT/US99/29549  
PRIOR FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-876-790-3

Query Match 25.2%; Score 55; DB 10; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 163  
DB 83 ILGVSKEFCLYCDKDKGSHPSLQKKEKMLAAQKESARRPFIFYRAQVS 137

RESULT 21  
US-10-139-833-13  
Sequence 13, Application US/10139833  
Publication No. US20030004106A1  
GENERAL INFORMATION:  
APPLICANT: Sarris, Christiaan M.  
APPLICANT: Giles, Jennifer  
APPLICANT: Mu, Sharon X.  
APPLICANT: Xia, Min  
APPLICANT: Baes, Michael B.  
APPLICANT: Craveiro, Roger  
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and  
TITLE OF INVENTION: Uses Thereof  
FILE REFERENCE: 00-1213-E  
CURRENT APPLICATION NUMBER: US/10/139,833  
CURRENT FILING DATE: 2002-05-06  
PRIOR APPLICATION NUMBER: 60/170,191  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: 60/188,053  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: 60/194,521  
PRIOR FILING DATE: 2000-04-04  
PRIOR APPLICATION NUMBER: 60/195,910

;; PRIOR FILING DATE: 2000-04-10  
;; PRIOR APPLICATION NUMBER: 09/724,583  
;; PRIOR FILING DATE: 2000-11-28  
;; NUMBER OF SEQ ID NOS: 37  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 13  
;; LENGTH: 192  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-139-833-13

Query Match 25.2%; Score 55; DB 14; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

## RESULT 22

US-10-888-918-3  
;; Sequence 3, Application US/10888918  
;; Publication No. US20040248187A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SIMS, John E.  
;; APPLICANT: SMITH, Dirk E.  
;; APPLICANT: BORN, Teresa L.  
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECC DNAS AND POLYPEPTI  
;; FILE REFERENCE: 2008-US  
;; CURRENT APPLICATION NUMBER: US/10/888,918  
;; PRIOR FILING DATE: 2004-07-09  
;; PRIOR APPLICATION NUMBER: US/09/876,790  
;; PRIOR FILING DATE: 2001-06-06  
;; PRIOR APPLICATION NUMBER: 60/112,163  
;; PRIOR FILING DATE: 1998-12-14  
;; PRIOR APPLICATION NUMBER: 60/146,675  
;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/29549  
;; PRIOR FILING DATE: 1999-12-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 192  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-888-918-3

Query Match 25.2%; Score 55; DB 16; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

## RESULT 23

US-10-888-867-3  
;; Sequence 3, Application US/10888867  
;; Publication No. US2005009075A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SIMS, John E.  
;; APPLICANT: SMITH, Dirk E.  
;; APPLICANT: BORN, Teresa L.  
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECC DNAS AND POLYPEPTI  
;; FILE REFERENCE: 2008-US  
;; CURRENT APPLICATION NUMBER: US/10/888,867  
;; PRIOR FILING DATE: 2004-07-09  
;; PRIOR APPLICATION NUMBER: US/09/876,790  
;; PRIOR FILING DATE: 2001-06-06  
;; PRIOR APPLICATION NUMBER: 60/112,163  
;; PRIOR FILING DATE: 1998-12-14

;; PRIOR APPLICATION NUMBER: 60/146,675  
;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/29549  
;; PRIOR FILING DATE: 1999-12-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 192  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-888-867-3

Query Match 25.2%; Score 55; DB 17; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

## RESULT 24

US-10-888-779-3  
;; Sequence 3, Application US/10888779  
;; Publication No. US2005009138A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SIMS, John E.  
;; APPLICANT: SMITH, Dirk E.  
;; APPLICANT: BORN, Teresa L.  
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECC DNAS AND POLYPEPTI  
;; FILE REFERENCE: 2008-US  
;; CURRENT APPLICATION NUMBER: US/10/888,779  
;; PRIOR FILING DATE: 2004-07-09  
;; PRIOR APPLICATION NUMBER: US/09/876,790  
;; PRIOR FILING DATE: 2001-06-06  
;; PRIOR APPLICATION NUMBER: 60/112,163  
;; PRIOR FILING DATE: 1998-12-14  
;; PRIOR APPLICATION NUMBER: 60/146,675  
;; PRIOR FILING DATE: 1999-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US99/29549  
;; PRIOR FILING DATE: 1999-12-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 3  
;; LENGTH: 192  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-888-779-3

Query Match 25.2%; Score 55; DB 17; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 83 ILIGVSKGEFCLYCDKDGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 137

## RESULT 25

US-10-888-780-3  
;; Sequence 3, Application US/10888780  
;; Publication No. US20050013797A1  
;; GENERAL INFORMATION:  
;; APPLICANT: SIMS, John E.  
;; APPLICANT: SMITH, Dirk E.  
;; APPLICANT: BORN, Teresa L.  
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECC DNAS AND POLYPEPTI  
;; FILE REFERENCE: 2008-US  
;; CURRENT APPLICATION NUMBER: US/10/888,780  
;; PRIOR FILING DATE: 2004-07-09  
;; PRIOR APPLICATION NUMBER: US/09/876,790  
;; PRIOR FILING DATE: 2001-06-06  
;; PRIOR APPLICATION NUMBER: 60/112,163



; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: 60/146,675  
 ; PRIOR FILING DATE: 1999-11-10  
 ; PRIOR APPLICATION NUMBER: PCT/US99/29549  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-888-780-3

Query Match 25.2%; Score 55; DB 17; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 5e-44;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAOKESARRPFIFYRAQVGS 163  
 Db 83 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAOKESARRPFIFYRAQVGS 137

RESULT 26  
 US-10-888-931-3  
 ; Sequence 3, Application US/10888931  
 ; Publication No. US20050013798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SIMS, John E.  
 ; APPLICANT: SMITH, Dirk E.  
 ; APPLICANT: BORN, Teresa L.  
 ; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECD DNAS AND POLYPEPTI  
 ; FILE REFERENCE: 2008-US  
 ; CURRENT APPLICATION NUMBER: US/10/888,931  
 ; CURRENT FILING DATE: 2004-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/876,790  
 ; PRIOR FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: 60/112,163  
 ; PRIOR FILING DATE: 1998-12-14  
 ; PRIOR APPLICATION NUMBER: 60/146,675  
 ; PRIOR FILING DATE: 1999-11-10  
 ; PRIOR APPLICATION NUMBER: PCT/US99/29549  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-888-931-3

Query Match 25.2%; Score 55; DB 17; Length 192;  
 Best Local Similarity 100.0%; Pred. No. 5e-44;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAOKESARRPFIFYRAQVGS 163  
 Db 83 ILGVSKGEFCLYCDKDGSHPSLQKKEKMLAOKESARRPFIFYRAQVGS 137

RESULT 27  
 US-10-006-867-142  
 ; Sequence 142, Application US/10006867  
 ; Publication No. US20020119130A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Matanabe, Colin K.  
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3230R1C1  
 ; CURRENT APPLICATION NUMBER: US/10/006,867  
 ; CURRENT FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: 60/063435  
 ; PRIOR FILING DATE: 1997-10-29  
 ; PRIOR APPLICATION NUMBER: 60/064215  
 ; PRIOR FILING DATE: 1997-10-29  
 ; PRIOR APPLICATION NUMBER: 60/082797  
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 ; PRIOR APPLICATION NUMBER: 60/083495  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/088021  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088029  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088030  
 ; PRIOR FILING DATE: 1998-06-04  
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 ; PRIOR FILING DATE: 1998-06-17  
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 ; PRIOR APPLICATION NUMBER: 60/090862  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091628  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/096012  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: 60/096757  
 ; PRIOR FILING DATE: 1998-08-17  
 ; PRIOR APPLICATION NUMBER: 60/096949  
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 ; PRIOR FILING DATE: 1998-08-26  
 ; PRIOR APPLICATION NUMBER: 60/098749  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: 60/099741  
 ; PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 60/099763  
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PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-22  
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PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
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PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
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PRIOR FILING DATE: 1998-10-27  
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PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106856  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108807  
PRIOR FILING DATE: 1998-11-17  
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PRIOR FILING DATE: 1998-12-15  
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PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/112854  
PRIOR FILING DATE: 1998-12-16  
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PRIOR FILING DATE: 1998-12-22  
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PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113430  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/114223  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 60/115614

PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/116527  
PRIOR FILING DATE: 1999-01-20  
PRIOR APPLICATION NUMBER: 60/116843  
PRIOR FILING DATE: 1999-01-22  
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PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/119287  
PRIOR FILING DATE: 1999-02-09  
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PRIOR FILING DATE: 1999-02-10  
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PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/120014  
PRIOR FILING DATE: 1999-02-11  
PRIOR APPLICATION NUMBER: 60/129122  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/129674  
PRIOR FILING DATE: 1999-04-16  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/144791  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/199397  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/380139  
PRIOR FILING DATE: 1998-08-25  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142

Query Match 25.2%; Score 55; DB 13; Length 193;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGPERCLYCDXKQSHPSLQKKKLMKLAQKESARRPIFYRAQVGS 163  
DB 84 ILGVSKGPERCLYCDXKQSHPSLQKKKLMKLAQKESARRPIFYRAQVGS 138

RESULT 28  
US-10-063-547-142  
Sequence 142, Application US/10063547  
Publication No. US20020182638A1  
GENERAL INFORMATION:  
APPLICANT: Baron, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 142  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-547-142

Query Match 25.2%; Score 55; DB 13; Length 193;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDGQSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
DB 84 ILGVSKGEFCLYCDKDGQSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 138

RESULT 29  
US-10-063-551-142  
; Sequence 142, Application US/10063551  
; Publication No. US20020183494A1  
; GENERAL INFORMATION:

; APPLICANT: Baton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,551  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 142  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-551-142

Query Match 25.2%; Score 55; DB 13; Length 193;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDGQSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
DB 84 ILGVSKGEFCLYCDKDGQSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 138

RESULT 30  
US-10-063-616-142  
; Sequence 142, Application US/10063616  
; Publication No. US20030013855A1  
; GENERAL INFORMATION:

; APPLICANT: Baton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,616  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 142

; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-616-142

Query Match 25.2%; Score 55; DB 14; Length 193;  
Best Local Similarity 100.0%; Pred. No. 5e-44;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDGQSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 163  
DB 84 ILGVSKGEFCLYCDKDGQSHPSLQKKEKMLAAQKESARRPFIYRAQVGS 138

Search completed: October 3, 2005, 11:50:26  
Job time : 166 secs

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OM protein - protein search, using sw model

Run on: October 3, 2005, 11:42:18 / Search time 16 Seconds  
(without alignments)  
1310.953 Million cell updates/sec

Title: US-10-694-978-2

Perfect score: 218  
Sequence: 1 MSFVGENSGVXMGSEDMEDK.....IEFSPQVCKAENSPSEVSD 218

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database :  
1: PIR\_79: \*  
2: p1r1: \*  
3: p1r2: \*  
4: p1r3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.7	413	2	H72606
2	8	3.7	982	2	T06576
3	8	3.7	993	2	T17230
4	8	3.7	1427	2	T39219
5	8	3.7	1622	2	D86428
6	8	3.7	2118	2	T13612
7	7	3.2	116	2	E72509
8	7	3.2	117	2	G87095
9	7	3.2	118	1	DNMTU3
10	7	3.2	118	1	DNMTU3
11	7	3.2	118	2	S71077
12	7	3.2	118	2	S71079
13	7	3.2	118	2	T09501
14	7	3.2	118	2	S70000
15	7	3.2	130	2	B72531
16	7	3.2	132	2	F96779
17	7	3.2	133	2	F71189
18	7	3.2	138	2	G97191
19	7	3.2	178	2	AB0264
20	7	3.2	179	2	AD2007
21	7	3.2	185	2	T49611
22	7	3.2	208	2	T52450
23	7	3.2	209	2	A75032
24	7	3.2	220	2	E72210
25	7	3.2	221	2	A72097
26	7	3.2	221	2	G86525
27	7	3.2	251	2	AC2187
28	7	3.2	265	2	T42957
29	7	3.2	290	2	H90001

30	7	3.2	301	2	T18788	hypothetical prote
31	7	3.2	303	2	E81348	binding-protein de
32	7	3.2	305	2	G70382	phosphoridylglyce
33	7	3.2	307	2	F69898	hypothetical prote
34	7	3.2	352	2	T51234	scarce-crow-like pr
35	7	3.2	356	2	C70025	multidrug-efflux t
36	7	3.2	366	2	T26038	hypothetical prote
37	7	3.2	367	2	C90399	iron-containing al
38	7	3.2	382	2	F82428	hypothetical prote
39	7	3.2	421	2	T02135	transcription enha
40	7	3.2	506	2	A40679	transcription enha
41	7	3.2	523	2	B40679	transcription enha
42	7	3.2	573	2	A86287	hypothetical prote
43	7	3.2	593	2	E86347	scarce-crow-like p
44	7	3.2	603	2	B96578	hypothetical prote
45	7	3.2	614	2	AB3596	periplasmic oligop
46	7	3.2	770	2	A12421	hypothetical prote
47	7	3.2	863	2	B64138	uridylyltransferas
48	7	3.2	946	2	S48255	probable membrane
49	7	3.2	964	2	T30455	hypothetical prote
50	7	3.2	1014	2	H86438	protein T19E23.7 l
51	7	3.2	1257	2	S28764	neurocan precursor
52	7	3.2	1268	2	S52781	neurocan - mouse
53	7	3.2	1609	2	S25345	probable membrane
54	7	3.2	2515	2	S47008	tenascin-like prot
55	7	3.2	2559	2	T09144	probable guanine n
56	7	3.2	2870	2	H96974	cyclic beta 1-2 gl
57	7	3.2	4056	2	H96599	protein P1416.10
58	7	2.8	14	2	PH0774	protein P1416.10
59	6	2.8	31	2	S49191	protein P1416.10
60	6	2.8	38	2	S32314	protein P1416.10
61	6	2.8	47	2	T29970	protein P1416.10
62	6	2.8	50	2	H82804	protein P1416.10
63	6	2.8	54	2	T07247	protein P1416.10
64	6	2.8	56	2	C83988	protein P1416.10
65	6	2.8	61	2	H83614	protein P1416.10
66	6	2.8	66	2	T15539	protein P1416.10
67	6	2.8	69	1	B56085	protein P1416.10
68	6	2.8	71	2	D81389	protein P1416.10
69	6	2.8	73	2	I77305	protein P1416.10
70	6	2.8	73	2	I77306	protein P1416.10
71	6	2.8	83	2	J01962	protein P1416.10
72	6	2.8	85	2	S68315	protein P1416.10
73	6	2.8	89	2	I69150	protein P1416.10
74	6	2.8	91	2	JS0036	protein P1416.10
75	6	2.8	94	2	B84281	protein P1416.10
76	6	2.8	96	2	AG1502	protein P1416.10
77	6	2.8	98	2	H84744	protein P1416.10
78	6	2.8	99	2	D81074	protein P1416.10
79	6	2.8	100	2	D71164	protein P1416.10
80	6	2.8	101	2	D70710	protein P1416.10
81	6	2.8	102	2	I53094	protein P1416.10
82	6	2.8	103	2	G72577	protein P1416.10
83	6	2.8	104	2	S17125	protein P1416.10
84	6	2.8	105	2	T46584	protein P1416.10
85	6	2.8	107	2	S07818	protein P1416.10
86	6	2.8	108	2	TS0348	protein P1416.10
87	6	2.8	111	2	D81780	protein P1416.10
88	6	2.8	114	2	A81204	protein P1416.10
89	6	2.8	114	2	S48982	protein P1416.10
90	6	2.8	117	2	E42519	protein P1416.10
91	6	2.8	117	2	D36850	protein P1416.10
92	6	2.8	117	2	T28562	protein P1416.10
93	6	2.8	117	2	B72166	protein P1416.10
94	6	2.8	118	2	S71081	protein P1416.10
95	6	2.8	118	2	B90259	protein P1416.10
96	6	2.8	120	2	T16510	protein P1416.10
97	6	2.8	128	2	C69195	protein P1416.10
98	6	2.8	123	2	H90389	protein P1416.10
99	6	2.8	123	2	C85835	protein P1416.10
100	6	2.8	125	2	AC0753	protein P1416.10
101	6	2.8	125	2	S78697	protein P1416.10
102	6	2.8	127	2	C85091	protein P1416.10

103	6	2.8	130	2	G72609	hypothetical prote
104	6	2.8	132	1	RS5814	ribosomal protein
105	6	2.8	132	1	T43826	ribosomal protein
106	6	2.8	132	2	F84322	50S ribosomal prot
107	6	2.8	132	2	I52524	testis lipid bindi
108	6	2.8	133	1	A47416	ubiquitin-like pro
109	6	2.8	133	2	A34248	ribosomal protein
110	6	2.8	133	2	PC4011	fatty acid-binding
111	6	2.8	133	2	T24099	hypothetical prote
112	6	2.8	133	2	P97840	hypothetical prote
113	6	2.8	133	2	I48346	ribosomal protein
114	6	2.8	134	2	D64558	hypothetical prote
115	6	2.8	134	2	F71949	hypothetical prote
116	6	2.8	136	2	T26814	hypothetical prote
117	6	2.8	137	2	E64845	ycdv protein - Esc
118	6	2.8	139	2	A83140	hypothetical prote
119	6	2.8	140	2	C71176	hypothetical prote
120	6	2.8	141	2	I48109	ferritin heavy cha
121	6	2.8	141	2	T17849	hypothetical prote
122	6	2.8	141	2	AC1994	hypothetical prote
123	6	2.8	141	2	A86417	probable auxin-ind
124	6	2.8	142	2	T30401	hypothetical prote
125	6	2.8	143	1	H69283	conserved hypotet
126	6	2.8	143	2	S04588	hemoglobin beta ch
127	6	2.8	144	2	S71764	naribonin (clone pN
128	6	2.8	145	2	S76877	hypothetical prote
129	6	2.8	146	1	HBRTF	hemoglobin beta ch
130	6	2.8	146	1	HBEMA	hemoglobin beta ch
131	6	2.8	146	1	HBFXB	hemoglobin beta ch
132	6	2.8	146	1	HBGP	hemoglobin beta ch
133	6	2.8	146	1	HBHY	hemoglobin beta ch
134	6	2.8	146	1	HBMSN1	hemoglobin beta ml
135	6	2.8	146	1	HBOSE	hemoglobin beta ch
136	6	2.8	146	1	HBTSM	hemoglobin beta ch
137	6	2.8	146	1	HBVOY	hemoglobin beta ch
138	6	2.8	146	1	HGBAY	hemoglobin gamma c
139	6	2.8	146	1	HGMQJ	hemoglobin gamma c
140	6	2.8	146	1	HGMQP	hemoglobin gamma c
141	6	2.8	146	2	A34947	hemoglobin beta ch
142	6	2.8	146	2	B29392	hemoglobin beta ch
143	6	2.8	146	2	B29391	hemoglobin beta ch
144	6	2.8	146	2	B25729	hemoglobin beta ch
145	6	2.8	146	2	B25359	hemoglobin beta ch
146	6	2.8	146	2	B24690	hemoglobin beta-S
147	6	2.8	146	2	JU0163	hemoglobin beta ch
148	6	2.8	146	2	S11398	PTS fructose-speci
149	6	2.8	147	1	I37025	hemoglobin gamma-G
150	6	2.8	147	1	HBMS	hemoglobin beta ma

## ALIGNMENTS

RESULT 1

H72606  
hypothetical protein APE1319 - Aeropyrum pernix (strain K1)

C/Species: Aeropyrum pernix  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C/Accession: H72606  
R/Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1  
A/Reference number: A72450; MUID:99310339; PMID:10382966

A/Accession: H72606  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-413 <KMA>  
A/Cross-references: UNIPROT:Q9YCD8; DDBJ:AP000061; NID:gs104821; PTDN:BA080310.1; PTD:cl  
A/Experimental source: strain K1  
C/Genetics:  
A/Gene: APE1319

Query Match 3.7%; Score 8; DB 2; Length 413;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 LASSLSA 101  
Db 12 LASSLSA 19

## RESULT 2

T06576  
probable protein kinase TCTR2 - tomato

C/Species: Lycopersicon esculentum (tomato)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T06576  
R/Hackett, R. M.  
submitted to the EMBL Data Library, March 1998

A/Reference number: Z15770  
A/Accession: T06576  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-982 <HAC>  
A/Cross-references: UNIPROT:O65833; EMBL:AJ005077; NID:e1296722; PTDN:CA006334.1; PTD:el  
A/Experimental source: cultivar Ailsa Craig  
C/Genetics:  
A/Gene: TCTR2

Query Match 3.7%; Score 8; DB 2; Length 982;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 ASSLSAS 102  
Db 30 ASSLSAS 37

## RESULT 3

T17230  
hypothetical protein DKFZp434E066.1 - human

C/Species: Homo sapiens (man)  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T17230  
R/Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999

A/Reference number: Z18722  
A/Accession: T17230  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-993 <ROE>  
A/Cross-references: UNIPROT:Q9UES6; EMBL:AL117432  
A/Experimental source: adult testis; clone DKFZp434E066  
C/Genetics:  
A/Note: DKFZp434E066.1

Query Match 3.7%; Score 8; DB 2; Length 993;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
Db 7 ALASSLS 14

## RESULT 4

T39219  
atp-binding cassette transporter abcl - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T39219  
R/McDonnell, R.; Barrett, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997

A/Reference number: Z21836  
A/Accession: T39219

A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-1427 <MCD>  
A:Cross-references: UNIPROT:Q92337; EMBL:Z99262; PIDD:CA16410.1; GSPDB:GN00066; SPDB:SI  
A:Experimental source: strain 972h-; cosmid C95  
C:Genetics:  
A:Gene: SPDB:SPAC9E9.12C  
A:Map position: 1  
C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1427;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

68 KVLVDSG 75  
|||||  
Db 1391 KVLVDSG 1398

RESULT 5

DB6428  
glutathione S-conjugate transporting ATPase (AtCKRP1) - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: DB6428  
R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.R.;  
ansen, N.F.; Hughes, B.; Hultzer, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maltl, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzbere, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A6141; MUID:21016719; PMID:11130712  
A:Accession: DB6428  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1622 <STO>  
C:Cross-references: UNIPROT:Q9C8G9; GB:AE005172; NID:g11055814; PIDD:AG28284.1; GSPDB:G  
C:Genetics:  
A:Map position: 1  
C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1622;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

68 KVLVDSG 75  
|||||  
Db 1440 KVLVDSG 1447

RESULT 6

T13612  
hypochemical protein 8D8.1 - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: T13612  
R:Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.  
submitted to the EMBL Data Library, April 1999  
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A:Reference number: Z17695  
A:Accession: T13612  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-2118 <PAP>  
A:Cross-references: UNIPROT:O76904; EMBL:AL022018; PIDD:CA17682.1  
C:Genetics:  
A:Cross-references: FlyBase:FBgn0024367  
A:introns: 47/3; 726/3; 770/1; 813/3; 1404/1; 1473/3  
A:Note: EG:8D8.1

```

C:Superfamily: Drosophila hypothetical protein Eg_898.1
Query Match      3.7%; Score 8; DB 2; Length 2118;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          96 SLSGSASA 103
|||||
Db          76 SLSGSASA 83

RESULT 7
E72509
probable non specific lipid-transfer protein APE2051 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Idate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72509
R:Kawarabayashi, Y., Hino, Y., Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamaya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawamura, Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: AY2450; MUID:99310339; PMID:10382966
A:Accession: E72509
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-116 <XAW>
A:Cross-references: UNIPROT:O9YA88; DDBJ:AP000063; NID:G5105654; PIDN:BAA81061.1; PID:d1c
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2051

Query Match      3.2%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          96 SLSGSAS 102
|||||
Db          39 SLSGSAS 45

RESULT 8
GB7095
conserved membrane protein ML1494 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Idate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: GB7095
R:Coile, S.T.; Sigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Horsfield, R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Felwell, T.; Frazer, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Native 409, 1007-1011, 2001
A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A>Title: Massive gene decay in the leprosy bacillus.
A:Reference number: AB6909; MUID:21128732; PMID:11234002
A:Accession: GB7095
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <STO>
A:Cross-references: UNIPROT:Q9CBX5; GB:AL450380; NID:G13093338; PIDN:CAC30444.1; GSPDB:GT
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1171

Query Match      3.2%; Score 7; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          108 LILIGVS 114
|||||
Db          98 LILIGVS 104

RESULT 9
DNW703
```

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - wheat mitochondrion  
C/Species: mitochondrion Triticum aestivum (common wheat)  
C/Date: 30-Jun-1992 #sequence\_revistion 14-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: JQ1374; S03609  
R/Guadaberto, J.M.; Bonnard, G.; Lamattina, L.; Grienenberger, J.M.  
Plant Cell 3, 1109-1120, 1991  
A/Title: Expression of the wheat mitochondrial nad3-rps12 transcription unit: correlatio  
A/Reference number: JQ1374; MUID:9233836; PMID:1726558  
A/Accession: JQ1374  
A/Molecule type: mRNA  
A/Residues: 1-118 <GUA>  
A/Cross-references: UNIPROT:P60160; GB:X59153; GB:S40874; NID:g433681  
A/Note: In plant mitochondria, RNA editing involves the conversion of C in the primary  
R/Note: this sequence is the translation of the consensus sequence of three cDNA clones  
R:Guadaberto, J.M.; Wintz, H.; Weill, J.H.; Grienenberger, J.M.  
Mol. Gen. Genet. 215, 118-127, 1988  
A/Title: The genes coding for subunit 3 of NADH dehydrogenase and for ribosomal protein  
A/Reference number: S03609; MUID:89201232; PMID:2853827  
A/Accession: S03609  
A/Molecule type: DNA  
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-45,'S',47-48,'S',50-63,'P',65-69,'P',7  
A/Cross-references: EMBL:X14262; NID:g13703; PIDD:CAA32475.1; PID:g13704  
C/Genetics:  
A/Gene: nad3  
A/Genome: mitochondrion  
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3  
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.2%; Score 7; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 STILLGV 113  
DB 18 STILLGV 24

RESULT 10  
DNZM2  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - maize mitochondrion  
C/Species: mitochondrion Zea mays (maize)  
C/Date: 30-Jun-1992 #sequence\_revistion 28-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: S70025; S70024; S05952  
R/Groskopf, D.; Mulligan, R.M.  
Curr. Genet. 29, 556-563, 1996  
A/Title: Developmental- and tissue-specificity of RNA editing in mitochondria of suspens  
A/Reference number: S70024; MUID:9626915; PMID:8662195  
A/Accession: S70025  
A/Molecule type: mRNA  
A/Residues: 1-118 <GRO>  
A/Cross-references: UNIPROT:P16265  
A/Experimental source: cultivar Black Mexican Sweet  
A/Note: In plant mitochondria, RNA editing involves the conversion of C in the primary  
A/Accession: S70024  
A/Molecule type: DNA  
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-45,'L',47-48,'S',50-61,'P',63,'P',65-6  
R/Guadaberto, J.M.; Wintz, H.; Weill, J.H.; Grienenberger, J.M.  
Mol. Gen. Genet. 215, 118-127, 1988  
A/Title: The genes coding for subunit 3 of NADH dehydrogenase and for ribosomal protein  
A/Reference number: S03609; MUID:89201232; PMID:2853827  
A/Accession: S05952  
A/Molecule type: DNA  
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-45,'S',47-48,'S',50-61,'P',63,'P',65-6  
A/Cross-references: EMBL:X14709; NID:g13913; PIDD:CAA32833.1; PID:g13914  
A/Experimental source: strain WF9-N  
A/Note: the authors translated the codon CCG for residue 62 as Leu  
C/Genetics:  
A/Gene: nad3  
A/Genome: mitochondrion  
C/Function:  
A/Pathway: respiratory chain  
A/Note: FAD cofactor

C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3  
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.2%; Score 7; DB 1; Length 118;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 STILLGV 113  
DB 18 STILLGV 24

RESULT 11  
S71077  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - common sunflower mitochondrion  
C/Species: mitochondrion Helianthus annuus (common sunflower)  
C/Date: 19-Mar-1997 #sequence\_revistion 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S71077; S71076  
R/Perrault, G.; Regina, T.M.R.; Ceci, L.R.; Quagliariello, C.  
Mol. Gen. Genet. 251, 326-337, 1996  
A/Title: Conservation of the organization of the mitochondrial nad3 and rps12 genes in e  
A/Reference number: S71076; MUID:96262185; PMID:8676875  
A/Accession: S71077  
A/Molecule type: mRNA  
A/Residues: 1-118 <PER>  
A/Cross-references: UNIPROT:P60159; EMBL:Z49775; NID:g1518349; PIDD:CAA89856.1; PID:g151  
A/Note: 2-Leu, 15-Leu, 21-Leu, 27-Leu, 70-Phe, 72-Leu, 77-Phe, 83-Ser, 89-Leu, 92-Phe, 10  
A/Accession: S71076  
A/Molecule type: DNA  
A/Residues: 1,'S',3-14,'P',16-20,'P',22-26,'P',28-69,'P',71,'P',73-76,'S',78-82,'P',84-8  
A/Cross-references: EMBL:Z49774; NID:g1518346; PIDD:CAA89854.1; PID:g1518347  
C/Genetics:  
A/Gene: nad3  
A/Genome: mitochondrion  
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3  
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.2%; Score 7; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 STILLGV 113  
DB 18 STILLGV 24

RESULT 12  
S71079  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Magnolia soulangeana mitochondrion  
C/Species: mitochondrion Magnolia soulangeana  
C/Date: 19-Mar-1997 #sequence\_revistion 09-May-1997 #text\_change 09-Jul-2004  
C/Accession: S71079; S71078  
R/Perrault, G.; Regina, T.M.R.; Ceci, L.R.; Quagliariello, C.  
Mol. Gen. Genet. 251, 326-337, 1996  
A/Title: Conservation of the organization of the mitochondrial nad3 and rps12 genes in e  
A/Reference number: S71076; MUID:96262185; PMID:8676875  
A/Accession: S71079  
A/Molecule type: mRNA  
A/Residues: 1-118 <PER>  
A/Cross-references: UNIPROT:Q96037; EMBL:Z49796; NID:g1518358; PIDD:CAA89888.1; PID:g151  
A/Note: 2-Leu, 5-Val, 15-Leu, 21-Leu, 42-Tyr, 46-Phe, 49-Phe, 62-Leu, 70-Phe, 72-  
A/Accession: S71078  
A/Molecule type: DNA  
A/Residues: 1,'S',3-4,'A',6-14,'P',16-20,'P',22-26,'P',28-41,'H',43-45,'S',47-48,'S',50-6  
A/Cross-references: EMBL:Z49797; NID:g1518355; PIDD:CAA89890.1; PID:g1518356  
C/Genetics:  
A/Gene: nad3  
A/Genome: mitochondrion  
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 3  
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.2%; Score 7; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 20;



RESULT 15  
B72531  
hypochemical protein APE2222 - *Aeropyrum pernix* (strain K1)  
C:Species: *Aeropyrum pernix*

```

RESULT 15
B72531
hypothetical protein APE2222 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B72531
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, Y.; Jin-no, K.; Takahashi, T.; Kudo, H.; Masuda, S.; Funahashi, T.; Tanaka, J.; Kudo, H.; Yamazaki, J.; Kato, H.; Takamiya, M.

```

DNA Res. 6, 83-101, 1999  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum*  
A:Reference number: A72450; MUID:99310339; PMID:10382966  
A:Accession: B72531

A:Molecule type: DNA  
A:Residues: 1-130 <KAM>  
A:Cross-references: UNIPROT:Q9Y9R6; DDBJ:AF000063; NID:G510554; PIDD:BAAB1234.1; PID:d1

A;Experimental source: strain K1  
C;Genetics:  
A;Gene: APE2222

Query Match	3.2%;	Score 7;	DB 2;	length 130;
Best Local Similarity	100.0%;	Pred. No. 21;		
Matches 7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 98 LSSASAE 104

Db 45 LSSASAE 51

RESULT 16  
F96779  
probable ribosomal protein S9 F9E10.17 [Imported] - Arabidopsis thaliana

CjDate: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
CjAccession: F96779  
P: Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
E.

Nature 40

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maici, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary

A/Residues: 1-132 <STO>

C/Genetics:  
A/Cena: F9F10 17

C:Superfamily: ribosomal protein s9/s16

Query Match 3.2%: Score 7: DB 2: Length 132:

```

Best Local Similarity 100.00, Freq. NO. 22,
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 94 LASSISS 100

```
Db      7 LASSISS 13
```

RESULT 17  
F71189

C:Species: *Pyrococcus horikoshii*  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
;Accession: F71189

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi, DNA Res. 5, 55-76, 1998  
 A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A:Reference number: A71000; PMID:98344137; PMID:9679194  
 A:Accession: F71189  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-133 <RAW>  
 A:Cross-references: UNIPROT:O59454; GB:AP000007; NID:g326134; PIDN:BAA30909.1; PID:g325  
 A:Experimental source: strain OT3  
 A>Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C:Genetics:  
 A:Gene: PH1790

Query Match 3.2%; Score 7; DB 2; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 SLSSAS 102  
 |||||  
 Db 68 SLSSAS 74

RESULT 18  
 G97191  
 Probable membrane protein [imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: G97191  
 R:Moiling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
 A:Reference number: A96900; PMID:21359325; PMID:21359325  
 A:Accession: G97191  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-138 <KUR>  
 A:Cross-references: UNIPROT:Q97GK0; GB:AE001437; PIDN:AAK80322.1; PID:g15025378; GSPDB:G  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC2366

Query Match 3.2%; Score 7; DB 2; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 GSLLIG 112  
 |||||  
 Db 30 GSLLIG 36

RESULT 19  
 JE0264  
 cyclin I - human  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: JE0264  
 R/Zhu, X.; Naz, R.K.  
 Biochem. Biophys. Res. Commun. 249, 56-60, 1998  
 A>Title: Expression of a novel isoform of cyclin I in human testis.  
 A:Reference number: JE0264; PMID:98381026; PMID:9705831  
 A:Accession: JE0264  
 A:Molecule type: mRNA  
 A:Residues: 1-178 <ZHU>  
 A:Cross-references: UNIPROT:Q14094  
 C:Comment: This protein may have a physiological role in spermatogenesis and/or human sp

Query Match 3.2%; Score 7; DB 2; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 PALASSL 98

Db 66 PALASSL 72  
 |||||

RESULT 20  
 AD2007  
 hypothetical protein all1610 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AD2007  
 R:Raneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat  
 A:Reference number: AB1807; PMID:21595285; PMID:11759840  
 A:Accession: AD2007  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-179 <KUR>  
 A:Cross-references: UNIPROT:O8YMK3; GB:BA000019; PIDN:BAW77976.1; PID:g17135430; GSPDB:G  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all1610

Query Match 3.2%; Score 7; DB 2; Length 179;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 SLILGV 113  
 |||||  
 Db 121 SLILGV 127

RESULT 21  
 T49611  
 hypothetical protein B3E4.240 [imported] - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
 C:Accession: T49611  
 R:Schulte, U.; Aign, V.; Hohnel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000  
 A:Reference number: Z25022  
 A:Accession: T49611  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-185 <SCH>  
 A:Cross-references: UNIPROT:Q9PSY8; EMBL:AJ355931; GSPDB:GN00116; NCSP:B3E4.240  
 A:Experimental source: BAC clone B3E4; strain OR74A  
 C:Genetics:  
 A:Gene: NCSP:B3E4.240  
 A:Map position: 6

Query Match 3.2%; Score 7; DB 2; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 SLSSASA 103  
 |||||  
 Db 34 SLSSASA 40

RESULT 22  
 T52450  
 ribosomal protein S9 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004  
 C:Accession: T52450  
 R:Arimura, S.; Takusagawa, S.; Hatano, S.; Nakazono, M.; Hirai, A.; Tsutsumi, N.  
 FEBS Lett. 450, 231-234, 1999  
 A>Title: A novel plant nuclear gene encoding chloroplast ribosomal protein S9 has a trans  
 A:Reference number: Z26079  
 A:Accession: T52450

A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-208 <ARN>  
A:Cross-references: UNIPROT:Q9XJ27; EMBL:AB022676; PIDD:BAA82396.1  
C:Genetics:  
A:Gene: rps9  
C:Superfamily: ribosomal protein S9/S16

Query Match 3.2%; Score 7; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 94 LASSLS 100  
DB 7 LASSLS 13

RESULT 23  
A75032  
hypothetical protein PAB1558 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: A75032  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: A75032  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-209 <RNA>  
A:Cross-references: UNIPROT:Q9UZA9; GB:AJ248287; GB:AL096836; NID:G5458657; PIDD:CA5015  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB1558

Query Match 3.2%; Score 7; DB 2; Length 209;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 52 VKSLNPK 58  
DB 193 VKSLNPK 199

RESULT 24  
E72210  
hypothetical protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: E72210  
R:Belson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A:Reference number: A72200; MUID:99287316; PMID:10360571  
A:Accession: E72210  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-220 <ARN>  
A:Cross-references: UNIPROT:Q9X2C0; GB:AE001817; GB:AE000512; NID:G4982370; PIDD:ADJ3686  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM1800

Query Match 3.2%; Score 7; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 164 RNMLESA 170  
DB 185 RNMLESA 191

RESULT 25  
A72097  
probable ABC transporter permease protein - Chlamydia pneumoniae (strain CWL029)  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: A72097  
R:Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: A72097  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-221 <ARN>  
A:Cross-references: UNIPROT:Q9Z8Q9; GB:AE001613; GB:AE001363; NID:G4376550; PIDD:ADJ1842;  
A:Experimental source: strain CWL029  
C:Genetics:  
A:Gene: CP0279  
C:Superfamily: ABC transporter permease protein

Query Match 3.2%; Score 7; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 53 KSLNPK 59  
DB 44 KSLNPK 50

RESULT 26  
G86525  
Probable ABC transporter permease protein [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G86525  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349; PMID:10871362  
A:Accession: G86525  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-221 <STO>  
A:Cross-references: UNIPROT:Q9Z8Q9; GB:BA000008; NID:G8978653; PIDD:BAA98489.1; GSPDB:GN  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: CP10279  
C:Superfamily: ABC transporter permease protein

Query Match 3.2%; Score 7; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

QY 53 KSLNPK 59  
DB 44 KSLNPK 50

RESULT 27  
AC2187  
Phospho-2-dehydro-3-deoxyphosphate aldolase/chorismate mutase [imported] - Nostoc sp. (st  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 16-Aug-2004  
C:Accession: AC2187  
R:Keneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AC2187

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-251 <KUR>  
 A:Cross-references: UNIPROT:Q8YSN4; GB:BA000019; PIDN:BAB74749.1; PID:G17132144; GSPDB:G  
 A:Experimental source: strain FCC 7120  
 C:Genetics:  
 A:Gene: alr3050  
 C:Superfamily: 2-dehydro-3-deoxyphosphoocetate aldolase

Query Match 3.2%; Score 7; DB 2; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 OVGSRM 166  
 DB 79 OVGSRM 85

## RESULT 28

T42957  
 hypothetical protein 42 - ateline herpesvirus 3 (strain 73)

C:Species: ateline herpesvirus 3  
 A:Variety: strain 73

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
 C:Accession: T42957

R:Albrecht, J.C.; Fleckenstein, B.  
 submitted to the EMBL Data Library, August 1998

A:Description: Primary structure of the herpesvirus ateles genome.

A:Reference number: Z22274

A:Accession: T42957  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-265 <ALB>

A:Cross-references: UNIPROT:Q9YTM3; EMBL:AF083424; PIDN:AAC95568.1  
 A:Experimental source: strain 73

C:Superfamily: hypothetical protein ORF42

Query Match 3.2%; Score 7; DB 2; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSX 115  
 DB 7 ILGVSX 13

RESULT 29  
 H90001  
 lipoprotein precursor [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C:Accession: H90001  
 R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001  
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: H90001  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-290 <KUR>

A:Cross-references: UNIPROT:Q99SG7; GB:BA000016; PID:G13701885; PIDN:BAB43177.1; GSPDB:G  
 A:Experimental source: strain N315

C:Genetics:  
 A:Gene: SAI893

C:Superfamily: stage III sporulation protein; stage III sporulation protein homology

Query Match 3.2%; Score 7; DB 2; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SLSSASA 103

DB 222 SLSSASA 228

## RESULT 30

T18788  
 hypothetical protein BE10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T18788  
 R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19022

A:Accession: T18788  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-301 <HIL>

A:Cross-references: UNIPROT:O17553; EMBL:Z93372; PIDN:CAB07546.1; GSPDB:GN00021; CESP:BE1

A:Experimental source: clone BE10  
 C:Genetics:  
 A:Gene: CESP:BE10.4  
 A:Map position: 3  
 A:Introns: 87/3; 147/3; 210/3; 256/3

Query Match 3.2%; Score 7; DB 2; Length 301;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SLSSASA 103  
 DB 101 SLSSASA 107

Search completed: October 3, 2005, 11:46:49  
 Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: October 3, 2005, 11:43:18 ; Search time 42 Seconds  
(without alignments)  
387.464 Million cell updates/sec

Title: US-10-694-978-2

Perfect score: 218  
Sequence: 1 MSFVGENSGVKGSEDEMKD.....IEFSPQVCKAEMSPSEVSD 218

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	218	100.0	218	4 US-09-398-412B-2	Sequence 2, Appli
2	55	25.2	115	3 US-09-128-155-5	Sequence 5, Appli
3	55	25.2	115	3 US-09-128-155-9	Sequence 9, Appli
4	55	25.2	115	3 US-09-128-155-13	Sequence 13, Appli
5	55	25.2	136	3 US-09-128-155-11	Sequence 11, Appli
6	55	25.2	167	3 US-09-128-155-7	Sequence 7, Appli
7	55	25.2	178	3 US-09-128-155-2	Sequence 2, Appli
8	55	25.2	218	3 US-09-293-625-2	Sequence 4, Appli
9	55	25.2	218	4 US-09-398-412B-4	Sequence 4, Appli
10	48	22.0	63	3 US-09-128-155-4	Sequence 8, Appli
11	37	17.0	52	3 US-09-128-155-8	Sequence 12, Appli
12	28	12.8	185	3 US-09-128-155-18	Sequence 12, Appli
13	14	6.4	21	3 US-09-364-206-12	Sequence 6, Appli
14	8	3.7	559	4 US-09-364-206-47	Sequence 47, Appli
15	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
16	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
17	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
18	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
19	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
20	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
21	8	3.7	651	3 US-08-972-927-6	Sequence 6, Appli
22	7	3.2	108	4 US-09-513-999C-5928	Sequence 5928, Ap
23	7	3.2	148	4 US-09-640-211A-790	Sequence 790, App
24	7	3.2	204	4 US-09-710-279-3240	Sequence 3240, App
25	7	3.2	221	4 US-09-158-452A-292	Sequence 292, App
26	7	3.2	224	4 US-09-438-185A-281	Sequence 281, App
27	7	3.2	254	4 US-09-796-149B-4	Sequence 4, Appli

28	7	3.2	264	4 US-09-107-532A-7009	Sequence 7009, Ap
29	7	3.2	272	4 US-09-252-991A-22707	Sequence 22707, A
30	7	3.2	310	4 US-09-270-767-41004	Sequence 41004, A
31	7	3.2	310	4 US-09-270-767-56220	Sequence 56220, A
32	7	3.2	326	4 US-09-248-796A-19891	Sequence 19891, A
33	7	3.2	349	4 US-09-248-796A-14572	Sequence 14572, A
34	7	3.2	352	4 US-09-265-585C-116	Sequence 116, App
35	7	3.2	352	4 US-09-265-585C-115	Sequence 115, App
36	7	3.2	353	3 US-09-186-276B-32	Sequence 32, Appli
37	7	3.2	353	4 US-08-842-445-32	Sequence 32, Appli
38	7	3.2	353	4 US-09-186-188B-32	Sequence 32, Appli
39	7	3.2	353	4 US-09-265-585C-32	Sequence 32, Appli
40	7	3.2	377	2 US-08-969-106-6	Sequence 6, Appli
41	7	3.2	377	3 US-09-054-492B-1	Sequence 1, Appli
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43	7	3.2	382	3 US-09-134-001C-4483	Sequence 4483, Ap
44	7	3.2	398	4 US-09-328-352-6770	Sequence 6770, Ap
45	7	3.2	424	4 US-09-489-039A-9628	Sequence 9628, Ap
46	7	3.2	452	4 US-09-540-236-2370	Sequence 2370, Ap
47	7	3.2	469	4 US-09-328-352-6276	Sequence 6276, Ap
48	7	3.2	487	4 US-09-107-532A-5219	Sequence 5219, Ap
49	7	3.2	553	4 US-09-902-540-14945	Sequence 14945, A
50	7	3.2	744	4 US-09-328-352-7920	Sequence 7920, Ap
51	7	3.2	749	4 US-09-949-016-8645	Sequence 8645, Ap
52	7	3.2	749	4 US-09-949-016-8646	Sequence 8646, Ap
53	7	3.2	749	4 US-09-949-016-8647	Sequence 8647, Ap
54	7	3.2	749	4 US-09-949-016-8648	Sequence 8648, Ap
55	7	3.2	766	4 US-09-949-016-11355	Sequence 11355, A
56	7	3.2	766	4 US-09-949-016-11356	Sequence 11356, A
57	7	3.2	766	4 US-09-949-016-11357	Sequence 11357, A
58	7	3.2	766	4 US-09-949-016-11358	Sequence 11358, A
59	7	3.2	1054	4 US-09-626-301-2	Sequence 2, Appli
60	7	3.2	1257	1 US-08-340-428B-49	Sequence 49, Appli
61	7	3.2	1257	4 US-09-358-092-886	Sequence 886, App
62	7	3.2	1258	4 US-09-358-092-886	Sequence 886, App
63	7	3.2	1729	4 US-09-134-000C-5675	Sequence 5675, Ap
64	6	2.8	25	3 US-09-049-691-57	Sequence 57, Appli
65	6	2.8	25	3 US-09-049-691-59	Sequence 59, Appli
66	6	2.8	25	3 US-09-049-691-62	Sequence 62, Appli
67	6	2.8	25	3 US-09-049-691-63	Sequence 63, Appli
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69	6	2.8	39	4 US-09-270-767-50105	Sequence 50105, A
70	6	2.8	43	4 US-09-674-973A-341	Sequence 341, App
71	6	2.8	44	4 US-09-674-973A-342	Sequence 342, App
72	6	2.8	47	4 US-09-902-540-13418	Sequence 13418, A
73	6	2.8	51	4 US-09-674-973A-345	Sequence 345, App
74	6	2.8	52	3 US-08-630-916A-71	Sequence 71, Appli
75	6	2.8	52	4 US-09-205-258-567	Sequence 567, App
76	6	2.8	52	4 US-09-674-973A-346	Sequence 346, App
77	6	2.8	60	4 US-09-328-352-7629	Sequence 7629, Ap
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79	6	2.8	62	4 US-09-270-767-40605	Sequence 40605, A
80	6	2.8	62	4 US-09-270-767-55821	Sequence 55821, A
81	6	2.8	62	4 US-09-248-796A-23629	Sequence 23629, A
82	6	2.8	63	4 US-09-543-681A-5842	Sequence 5842, Ap
83	6	2.8	67	2 US-08-588-258B-6	Sequence 6, Appli
84	6	2.8	67	3 US-08-460-505-6	Sequence 6, Appli
85	6	2.8	67	5 PCT-US96-08295-6	Sequence 6, Appli
86	6	2.8	70	4 US-09-270-767-33965	Sequence 33965, A
87	6	2.8	70	4 US-09-270-767-49182	Sequence 49182, A
88	6	2.8	74	4 US-09-248-796A-20872	Sequence 20872, A
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90	6	2.8	75	4 US-09-489-039A-14009	Sequence 14009, A
91	6	2.8	75	4 US-09-270-767-40442	Sequence 40442, A
92	6	2.8	78	4 US-09-270-767-55658	Sequence 55658, A
93	6	2.8	78	4 US-09-489-039A-13889	Sequence 13889, A
94	6	2.8	78	4 US-09-134-000C-6321	Sequence 6321, Ap
95	6	2.8	78	4 US-09-583-110-2668	Sequence 2668, Ap
96	6	2.8	79	4 US-09-304-615-167	Sequence 3202, Ap
97	6	2.8	79	4 US-09-543-681A-6548	Sequence 6548, App
98	6	2.8	79	4 US-09-248-796A-26832	Sequence 26832, A
99	6	2.8	80	4 US-09-304-615-120	Sequence 120, App
100	6	2.8	81	4 US-09-543-681A-5027	Sequence 5027, Ap

101 6 2.8 82 4 US-09-621-976-5315 Sequence 5315, Ap  
102 6 2.8 82 4 US-09-621-976-5321 Sequence 5321, Ap  
103 6 2.8 84 4 US-09-107-433-4129 Sequence 4129, Ap  
104 6 2.8 85 4 US-09-543-681A-8234 Sequence 8234, Ap  
105 6 2.8 86 4 US-09-270-767-57072 Sequence 57072, A  
106 6 2.8 87 4 US-09-248-796A-22328 Sequence 22328, A  
107 6 2.8 88 4 US-09-489-039A-9865 Sequence 9865, Ap  
108 6 2.8 91 1 US-08-455-896-8 Sequence 8, Ap11  
109 6 2.8 91 2 US-08-933-149-8 Sequence 8, Ap11  
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114 6 2.8 91 4 US-09-509-015-8 Sequence 8, Ap11  
115 6 2.8 91 4 US-09-270-767-39508 Sequence 39508, A  
116 6 2.8 91 4 US-09-270-767-54725 Sequence 54725, A  
117 6 2.8 91 5 PCT-US96-08235-8 Sequence 8, Ap11  
118 6 2.8 93 4 US-09-248-796A-26322 Sequence 26322, A  
119 6 2.8 94 4 US-09-949-016-10599 Sequence 10599, A  
120 6 2.8 99 4 US-09-540-236-2992 Sequence 2992, Ap  
121 6 2.8 100 4 US-09-513-999C-4593 Sequence 4593, Ap  
122 6 2.8 104 4 US-09-513-999C-6549 Sequence 6549, Ap  
123 6 2.8 105 4 US-09-583-110-4875 Sequence 4875, Ap  
124 6 2.8 106 3 US-09-199-637A-283 Sequence 283, Ap  
125 6 2.8 111 4 US-09-270-767-61594 Sequence 61594, A  
126 6 2.8 113 4 US-09-513-999C-4899 Sequence 4899, Ap  
127 6 2.8 114 1 US-08-040-548-4 Sequence 4, Ap11  
128 6 2.8 114 1 US-08-466-344-4 Sequence 4, Ap11  
129 6 2.8 115 4 US-09-248-796A-27123 Sequence 27123, A  
130 6 2.8 118 4 US-09-765-815-8 Sequence 8, Ap11  
131 6 2.8 118 4 US-09-311-021-158 Sequence 158, Ap  
132 6 2.8 120 3 US-08-890-865A-14 Sequence 14, Ap11  
133 6 2.8 120 4 US-09-621-976-5313 Sequence 5313, Ap  
134 6 2.8 122 4 US-09-461-325-355 Sequence 355, Ap  
135 6 2.8 122 4 US-10-012-542-355 Sequence 355, Ap  
136 6 2.8 122 4 US-10-115-123-355 Sequence 355, Ap  
137 6 2.8 122 4 US-09-902-540-11364 Sequence 11364, A  
138 6 2.8 128 3 US-09-134-001C-3090 Sequence 3090, Ap  
139 6 2.8 128 4 US-09-205-258-279 Sequence 279, Ap  
140 6 2.8 128 4 US-09-270-767-31764 Sequence 31764, A  
141 6 2.8 128 4 US-09-270-767-46981 Sequence 46981, A  
142 6 2.8 131 1 US-08-409-731A-7 Sequence 7, Ap11  
143 6 2.8 131 2 US-08-470-298B-7 Sequence 7, Ap11  
144 6 2.8 132 2 US-08-470-298B-12 Sequence 12, Ap11  
145 6 2.8 132 4 US-09-732-210-589 Sequence 589, Ap  
146 6 2.8 132 4 US-09-732-210-590 Sequence 590, Ap  
147 6 2.8 133 2 US-08-820-825-11 Sequence 11, Ap11  
148 6 2.8 133 2 US-09-023-073A-7 Sequence 7, Ap11  
149 6 2.8 133 3 US-09-307-817-11 Sequence 11, Ap11  
150 6 2.8 133 3 US-09-361-737-7 Sequence 7, Ap11

## ALIGNMENTS

RESULT 1  
US-09-398-412B-2  
Sequence 2, Application US/09398412B  
Patent No. 6680380  
GENERAL INFORMATION:  
APPLICANT: Tians, Jacqueline C.  
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reags  
TITLE OF INVENTION: methods  
FILE REFERENCE: DX0904K  
CURRENT APPLICATION NUMBER: US/09/398, 412B  
CURRENT FILING DATE: 1999-09-17  
PRIOR APPLICATION NUMBER: US 60/100948  
PRIOR FILING DATE: 1998-09-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 218  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-398-412B-2  
Query Match 100.0%; Score 218; DB 4; Length 218;  
Best Local Similarity 100.0%; Pred. No. 2,1e+208;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSFVGENSVKMGSEDEWDEPOCCIEDPAGPLEBGPPLPMNRYHYSRKYSINPKKF 60  
DB 1 MSFVGENSVKMGSEDEWDEPOCCIEDPAGPLEBGPPLPMNRYHYSRKYSINPKKF 60  
QY 61 SHHDQHKVLVDSGNTLIVPDKNYRPIFFALASSLSASAEKGSLLIGVSGEFCL 120  
DB 61 SHHDQHKVLVDSGNTLIVPDKNYRPIFFALASSLSASAEKGSLLIGVSGEFCL 120  
QY 121 YCDKXGSHPSLQLKKEKMLAAQKESARRPIFYRAQVGRNMLESAHPGFICT 180  
DB 121 YCDKXGSHPSLQLKKEKMLAAQKESARRPIFYRAQVGRNMLESAHPGFICT 180  
QY 181 CNCNEPVGYTDKFNKRKHIEFSFQPYCKAEMSPSEVSD 218  
DB 181 CNCNEPVGYTDKFNKRKHIEFSFQPYCKAEMSPSEVSD 218

RESULT 2  
US-09-128-155-5  
Sequence 5, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-5

Query Match 25.2%; Score 55; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 8.4e+47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 109 ILLGVSGEFCLYCDKXGSHPSLQLKKEKMLAAQKESARRPIFYRAQVGS 163  
DB 6 ILLGVSGEFCLYCDKXGSHPSLQLKKEKMLAAQKESARRPIFYRAQVGS 60

RESULT 3  
US-09-128-155-9  
Sequence 9, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 9  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-9

Query Match 25.2%; Score 55; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 8.4e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 60

RESULT 4  
US-09-128-155-13  
Sequence 13, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-13

Query Match 25.2%; Score 55; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 8.4e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 6 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 60

RESULT 5  
US-09-128-155-11  
Sequence 11, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 136  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-11

Query Match 25.2%; Score 55; DB 3; Length 136;  
Best Local Similarity 100.0%; Pred. No. 9.8e-47;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 27 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 81

RESULT 6  
US-09-128-155-7  
Sequence 7, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 167  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-7

Query Match 25.2%; Score 55; DB 3; Length 167;  
Best Local Similarity 100.0%; Pred. No. 1.2e-46;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 58 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 112

RESULT 7  
US-09-128-155-2  
Sequence 2, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 178  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-2

Query Match 25.2%; Score 55; DB 3; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.2e-46;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163  
DB 69 ILGVSKGEFCLYCDKDKGSHPSLQKKKMKLAQKESARRPFIYRAQVGS 123

RESULT 8  
US-09-293-625-2  
Sequence 2, Application US/09293625

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/ Patent No. 6342371
/ GENERAL INFORMATION:
/ APPLICANT: Young, Peter R.
/ APPLICANT: McDonnell, Peter C
/ TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
/ FILE REFERENCE: GP-70607
/ CURRENT APPLICATION NUMBER: US/09/293,625
/ CURRENT FILING DATE: 1999-04-16
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-293-625-2

Query Match      25.2%; Score 55; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB      109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163

RESULT 9
US-09-398-412B-4
/ Sequence 4, Application US/09398412B
/ Patent No. 6680380
/ GENERAL INFORMATION:
/ APPLICANT: Tlman, Jacqueline C.
/ TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
/ FILE REFERENCE: DX0904K
/ CURRENT APPLICATION NUMBER: US/09/398,412B
/ CURRENT FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: US 60/100948
/ PRIOR FILING DATE: 1998-09-18
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 4
/ LENGTH: 218
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-398-412B-4

Query Match      25.2%; Score 55; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163
DB      109 ILGVSKGEFCLYCDKDKGQSHPSLQKKKMKLAQKESARRPFIYRAQVGS 163

RESULT 10
US-09-128-155-4
/ Sequence 4, Application US/09128155
/ Patent No. 6117654
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
/ FILE REFERENCE: 09404/052001
/ CURRENT APPLICATION NUMBER: US/09/128,155
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 60/091,650
/ EARLIER FILING DATE: 1998-07-02
/ EARLIER APPLICATION NUMBER: US 60/054,646
/ EARLIER FILING DATE: 1997-08-04
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ OTHER INFORMATION: interest in a stretch of genomic DNA
```

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/ LENGTH: 63
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-128-155-4

Query Match      22.0%; Score 48; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.3e-40;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSPVGENSGVKMGSEDMKDEPQCCLEDPAGSPLEPGSLPTMNFVHT 48
DB      1 MSPVGENSGVKMGSEDMKDEPQCCLEDPAGSPLEPGSLPTMNFVHT 48

RESULT 11
US-09-128-155-8
/ Sequence 8, Application US/09128155
/ Patent No. 6117654
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
/ FILE REFERENCE: 09404/052001
/ CURRENT APPLICATION NUMBER: US/09/128,155
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 60/091,650
/ EARLIER FILING DATE: 1998-07-02
/ EARLIER APPLICATION NUMBER: US 60/054,646
/ EARLIER FILING DATE: 1997-08-04
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-128-155-8

Query Match      17.0%; Score 37; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 MGSEDMKDEPQCCLEDPAGSPLEPGSLPTMNFVHT 48
DB      1 MGSEDMKDEPQCCLEDPAGSPLEPGSLPTMNFVHT 37

RESULT 12
US-09-128-155-18
/ Sequence 18, Application US/09128155
/ Patent No. 6117654
/ GENERAL INFORMATION:
/ APPLICANT: Pan, Yang
/ TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
/ FILE REFERENCE: 09404/052001
/ CURRENT APPLICATION NUMBER: US/09/128,155
/ CURRENT FILING DATE: 1998-08-03
/ EARLIER APPLICATION NUMBER: US 60/091,650
/ EARLIER FILING DATE: 1998-07-02
/ EARLIER APPLICATION NUMBER: US 60/054,646
/ EARLIER FILING DATE: 1997-08-04
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 18
/ LENGTH: 185
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ NAME/KEY: synthetically generated
/ LOCATION: (1)...(185)
/ OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
/ OTHER INFORMATION: interest in a stretch of genomic DNA
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FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(185)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-128-155-18

Query Match 12.8%; Score 28; DB 3; Length 185;  
Best Local Similarity 100.0%; Pred. No. 8.3e-20;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILGVSKGEFCYCDKKGSHPSLOLK 136  
Db 86 ILGVSKGEFCYCDKKGSHPSLOLK 113

RESULT 13  
US-09-128-155-12  
Sequence 12, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Pan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
CURRENT FILING DATE: 1998-08-03  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/054,646  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-128-155-12

Query Match 6.4%; Score 14; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 9.2e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 IFFALASSLSASA 103  
Db 8 IFFALASSLSASA 21

RESULT 14  
US-09-364-206-47  
Sequence 47, Application US/09364206  
Patent No. 6475752  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Baugh, Mariah R.  
APPLICANT: Kaefer, Matthew R.  
TITLE OF INVENTION: Mammalian Imidazole Receptor  
FILE REFERENCE: PC-0006 US  
CURRENT APPLICATION NUMBER: US/09/364,206  
CURRENT FILING DATE: 1999-07-30  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PERL Program  
SEQ ID NO 47  
LENGTH: 559  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY:  
OTHER INFORMATION: W43396  
PUBLICATION INFORMATION:  
US-09-364-206-47

Query Match 3.7%; Score 8; DB 4; Length 559;

Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
Db 106 ALASSLS 113

RESULT 15  
US-08-650-766-6  
Sequence 6, Application US/08650766D  
Patent No. 6015690  
GENERAL INFORMATION:  
APPLICANT: PILETZ, John E.  
APPLICANT: IVANOV, Tina R.  
TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND  
FILE REFERENCE: Corrected Sequence Listing  
Patent No. 6015690  
CURRENT APPLICATION NUMBER: US/08/650,766D  
CURRENT FILING DATE: 1996-05-20  
EARLIER APPLICATION NUMBER: US 60/012,600  
EARLIER FILING DATE: 1996-03-01  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 651  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-650-766-6

Query Match 3.7%; Score 8; DB 3; Length 651;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
Db 106 ALASSLS 113

RESULT 16  
US-08-922-635-5  
Sequence 5, Application US/08922635A  
Patent No. 6033871  
GENERAL INFORMATION:  
APPLICANT: PILETZ, John E.  
APPLICANT: IVANOV, Tina R.  
TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDAZOLINE RECEPTIVE POLYPEPTIDES  
FILE REFERENCE: Corrected Sequence Listing  
Patent No. 6033871  
CURRENT APPLICATION NUMBER: US/08/922,635A  
CURRENT FILING DATE: 1997-09-03  
EARLIER APPLICATION NUMBER: 08/650,766  
EARLIER FILING DATE: 1996-05-20  
EARLIER APPLICATION NUMBER: 60/012,600  
EARLIER FILING DATE: 1996-03-01  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 651  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-922-635-5

Query Match 3.7%; Score 8; DB 3; Length 651;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
Db 106 ALASSLS 113

```
RESULT 17
US-09-389-487-6
; Sequence 6, Application US/09389487
; Patent No. 6576742
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6576742
; CURRENT APPLICATION NUMBER: US/09/389,487
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: US 08/650,766
; EARLIER FILING DATE: 1996-05-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-389-487-6

Query Match      3.7%; Score 8; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 ALASSISS 100
Db      106 ALASSISS 113

RESULT 18
US-08-922-635-22
; Sequence 22, Application US/08922635A
; Patent No. 6033871
; GENERAL INFORMATION:
; APPLICANT: PILETZ, John E.
; APPLICANT: IVANOV, Tina R.
; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
; FILE REFERENCE: Corrected Sequence Listing
; Patent No. 6033871
; CURRENT APPLICATION NUMBER: US/08/922,635A
; CURRENT FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 08/650,766
; EARLIER FILING DATE: 1996-05-20
; EARLIER APPLICATION NUMBER: 60/012,600
; EARLIER FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-922-635-22

Query Match      3.7%; Score 8; DB 3; Length 1070;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 ALASSISS 100
Db      84 ALASSISS 91

RESULT 19
US-09-364-206-2
; Sequence 2, Application US/09364206
; Patent No. 6475752
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
```

```
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baugh, Mariah R.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: Mammalian Imidazoline Receptor
; FILE REFERENCE: PC-0006 US
; CURRENT APPLICATION NUMBER: US/09/364,206
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1504
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
; OTHER INFORMATION: 129581CD1
; PUBLICATION INFORMATION:
US-09-364-206-2

Query Match      3.7%; Score 8; DB 4; Length 1504;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 ALASSISS 100
Db      518 ALASSISS 525

RESULT 20
US-08-972-927-6
; Sequence 6, Application US/08972927
; Patent No. 6166290
; GENERAL INFORMATION:
; APPLICANT: Rea, Philip A
; APPLICANT: Lu, Yu-ping
; APPLICANT: Li, Ze-Sheng
; TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: One Commerce Square, 2005 Market Street, 22nd
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,927
; FILING DATE: 18-NOV-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,040
; FILING DATE: 18-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/061,328
; FILING DATE: 08-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Doyle Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-1202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 amino acids
```

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-972-927-6

Query Match 3.2%; Score 8; DB 3; Length 1622;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 KVLVDSG 75  
Db 1440 KVLVDSG 1447

RESULT 21  
US-09-107-532A-6620  
Sequence 6620, Application US/09107532A  
Patent No. 6583275

GENERAL INFORMATION:  
APPLICANT: Lynn A Doucetere-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998

ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 6620:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...73  
SEQUENCE DESCRIPTION: SEQ ID NO: 6620:  
US-09-107-532A-6620

Query Match 3.2%; Score 7; DB 4; Length 73;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 SSLSAS 102  
Db 39 SSLSAS 45

RESULT 22  
US-09-513-999C-5928  
Sequence 5928, Application US/09513999C  
Patent No. 6783961

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59 US2,REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 5928  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-513-999C-5928

Query Match 3.2%; Score 7; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DSGNLIA 79  
Db 31 DSGNLIA 37

RESULT 23  
US-09-640-211A-790  
Sequence 790, Application US/09640211A  
Patent No. 6833446

GENERAL INFORMATION:  
APPLICANT: Wood, Marion  
APPLICANT: Shenk, Michael A.  
APPLICANT: McGrath, Annette  
APPLICANT: Glenn, Matthew  
TITLE OF INVENTION: Modifications and Methods for the  
FILE REFERENCE: 11000.1021CIU  
CURRENT APPLICATION NUMBER: US/09/640,211A  
CURRENT FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 2368  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 790  
LENGTH: 148  
TYPE: PRT  
ORGANISM: Eucalyptus grandis

US-09-640-211A-790

Query Match 3.2%; Score 7; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 ASSLSA 101  
Db 20 ASSLSA 26

RESULT 24  
US-09-710-279-3240  
Sequence 3240, Application US/09710279  
Patent No. 6703492

GENERAL INFORMATION:  
APPLICANT: KIMMERLY, WILLIAM JOHN  
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3240  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-09-710-279-3240

Query Match 3.2%; Score 7; DB 4; Length 204;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 KVKSLNP 57  
|||  
Db 82 KVKSLNP 88

RESULT 25  
US-09-198-452A-292  
; Sequence 292, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 292  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-292

Query Match 3.2%; Score 7; DB 4; Length 221;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KSLNPKK 59  
|||  
Db 44 KSLNPKK 50

RESULT 26  
US-09-438-185A-281  
; Sequence 281, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kaiman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 281

; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: Cpn0279  
US-09-438-185A-281

Query Match 3.2%; Score 7; DB 4; Length 224;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KSLNPKK 59  
|||  
Db 47 KSLNPKK 53

RESULT 27  
US-09-796-149B-4  
; Sequence 4, Application US/09796149B  
; Patent No. 6825033  
; GENERAL INFORMATION:  
; APPLICANT: Univ. of Southern California  
; TITLE OF INVENTION: Mutated cyclin G1 protein  
; FILE REFERENCE: 4-31342A/USC  
; CURRENT APPLICATION NUMBER: US/09/796,149B  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-149B-4

Query Match 3.2%; Score 7; DB 4; Length 254;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FALASSL 98  
|||  
Db 27 FALASSL 33

RESULT 28  
US-09-107-532A-7009  
; Sequence 7009, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277  
 INFORMATION FOR SEQ ID NO: 7009:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 264 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (B) LOCATION 1..264  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7009:  
 US-09-107-532A-7009

Query Match 3.2%; Score 7; DB 4; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 QLKKEKL 140  
 |||||  
 Db 251 QLKKEKL 257

RESULT 29  
 US-09-252-991A-22707  
 ; Sequence 22707, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 22707  
 ; LENGTH: 272  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-22707

Query Match 3.2%; Score 7; DB 4; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 VLVLDSG 75  
 |||||  
 Db 14 VLVLDSG 20

RESULT 30  
 US-09-270-767-41004  
 ; Sequence 41004, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 41004  
 ; LENGTH: 310  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 US-09-270-767-41004

Query Match 3.2%; Score 7; DB 4; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 LILGVGS 114  
 |||||  
 Db 195 LILGVGS 201

Search completed: October 3, 2005, 11:47:36  
 Job time : 45 secs

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